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Run on: March 1, 2001, 16:22:04 ;	Search time 88.16 Seconds (without alignments) 37.226 Million cell updates/sec
Title: US-09-331-631A-32	Perfect score: 76
Sequence: 1 CXXCXXXCXXXXXXCXXXCXXXC 28	Scoring table: BLOSUM62DX Gapop 10.0 , Gapext 0.5
Searched: 374700 seqs, 11707915 residues	Total number of hits satisfying chosen parameters: 374700
Minimum DB seq length: 0	Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%	Maximum Match 100%
Database : Listing first 45 summaries	
	1: SPTREMBL15:*
	2: sp_archea:*
	3: sp_bacteria:*
	4: sp_fungi:*
	5: sp_invertebrate:*
	6: sp_mammal:*
	7: sp_mhc:*
	8: sp_organelle:*
	9: sp_phage:*
	10: sp_plant:*
	11: sp_rabbit:*
	12: sp_virus:*
	13: sp_vertebrate:*
	14: sp_unclassified:*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES
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	2: sp_bacteria:*
	3: sp_fungi:*
	4: sp_invertebrate:*
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	7: sp_organelle:*
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RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R.,  
 RA Palacio M., Pittman G.S., Pan S., Pollard J., Pur-  
 RA Reiner K., Remington K., Saunders R.D.C., Scheeler  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R.,  
 RA Svistak R., Tector C., Turner R., Venter E., Wang  
 RA Wang Z.-Y., Wasserman D.A., Weinstock M.G., Weissman  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang  
 RA ye J., Yeh R.-F., Zaveri J.S., Zhang M., Zhang G., Z-  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
 RA "The genome sequence of *Drosophila melanogaster*,"  
 RL *Science* 287:2185-2195 (2000).  
 DR EBL1; AF003672; AA05424-1.  
 DR FB910004173; Mst84Db.  
 DR IMPERPRO; IPR010150; -.  
 DR PROSITE; PS0198; 4FE4S\_FERREDOXIN; UNKNOWN\_4.  
 SQ SEQUENCE 74 AA; 6725 MW; CC64FF0F7A7E7CABC CRC64

Pacileb J.M.,  
i v., Reese M.G.,  
F., Shen H.,  
.., Smith T.,  
.., Sun E.,  
A.H., Wang X.,  
bach J.,  
S., Yao Q.A.,  
nao Q., zheng L.,  
Zhu X., Smith H.O.,

DR PROSITE; PS01208; WFWC; UNKNOWN\_1.  
 SQ SEQUENCE: 152 AA; 15645 MW; 6E254F0BE476D354 CRC64;

Query Match 100.0%; Score 76; DB 5; Length 152;  
 Best Local Similarity 21.4%; Pred. No. 15;  
 Matches 6; Conservative 22; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXCXXXXCXXXXXXCXXXXCXXXXCXXXXC 28  
 QY 1 ::::::::::::::::::::: 1 :::::::  
 Db 91 CCCCCRCCCTCCRCCCTRCCTCCRPCC 118

RESULT 4  
 ID 022048 PRELIMINARY; PRT; 164 AA.  
 AC 022048  
 DT 01-NOV-1996 (TREMBREL. 01, Created)  
 DT 01-NOV-1996 (TREMBREL. 01, Last sequence update)  
 DT 01-MAY-2000 (TREMBREL. 13, Last annotation update)  
 DE T01B7.8 PROTEIN.  
 GN T01B7.8  
 OS Caenorhabditis elegans.  
 OC Rhabditidae; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Pelodoridae; Caenorhabditis.  
 OC Rhabditidae; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Pelodoridae; Caenorhabditis.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RX MEDLINE=94150718; PubMed=7906398;  
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,  
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,  
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,  
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,  
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,  
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,  
 RA Parsons J., Percy C., Saunders D., Saunders L., Roopa R., Shownkeen R.,  
 RA Smalton N., Smith A., Sonnhammer E., Staden R., Sulston J.,  
 RA Thiberry Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,  
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,  
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
 RT elegans.", Nature 368:32-38 (1994).  
 RL [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RA Nhan M.;  
 RL Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RA Waterston R.;  
 RL Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; U58760; AAB07010.1; -.  
 DR INTERPRO; IPR001007; -.  
 DR INTERPRO; IPR001271; -.  
 DR INTERPRO; IPR001450; -.  
 DR PROSITE; PS00198; 4FEAS.FERREDOXIN; UNKNOWN\_1.  
 DR PROSITE; PS00269; DEFENSIN; 1.  
 DR PROSITE; PS01208; WFWC; UNKNOWN\_1.  
 SQ SEQUENCE: 188 AA; 18978 MW; 0C5DD0C5CABE0C4B CRC64;

Query Match 100.0%; Score 76; DB 5; Length 188;  
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 Matches 6; Conservative 22; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXCXXXXCXXXXXXCXXXXCXXXXCXXXXC 28  
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 Db 92 CCCCCRCCCTCCRCCCTRCCTCCRPCC 119

RESULT 6  
 ID 039566 PRELIMINARY; PRT; 413 AA.  
 AC 039566;  
 DT 01-NOV-1996 (TREMBREL. 01, Created)  
 DT 01-NOV-1996 (TREMBREL. 01, Last sequence update)  
 DE (HIV-6) 01102; VARIANT A DNA, COMPLETE VIRION GENOME.  
 GN U88  
 OS Human herpesvirus 6.  
 OC DNA viruses, no RNA stage; Herpesviridae;  
 OC Betaherpesvirinae; Roseolovirus.  
 OC NCBI\_TaxID=10368;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=U1102; VARIANT A;  
 RX MEDLINE=95206321; PubMed=7747482;  
 RA Compells U.A., Nicholas J., Lawrence G., Jones M., Thomson B.J.,  
 RA Martin M.E., Efstathiou S., Craxton M., Macaulay H.A.;  
 DT 01-NOV-1996 (TREMBREL. 01, Last sequence update)  
 "The DNA sequence of human herpesvirus-6: structure, coding content,

- RT and genome evolution";  
RL virology 209:29-51(1995).  
RN [2]
- SEQUENCE FROM N.A.  
RN STRAIN=U1102; VARIANT A;  
RC MEDLINE=90080132; PubMed=2152817;  
RA Barrell B.G.; Lawrence G.L., Chee M., Craxton M.A., Gompels U.A., Honess R.W.,  
RA Barrell B.G.; Lawrence G.L., Chee M., Craxton M.A., Gompels U.A., Honess R.W.,  
RT "Human herpesvirus 6 is closely related to human cytomegalovirus.";  
RL J. Virol. 64:287-299(1990).  
RN [3]
- SEQUENCE FROM N.A.  
RN STRAIN=U1102; VARIANT A;  
RC MEDLINE=91237802; PubMed=1851860;  
RA Chang C.K., Balachandran N.;  
RT "Identification, characterization, and sequence analysis of a cDNA  
encoding a phosphoprotein of human herpesvirus 6.;"  
RL J. Virol. 65:2884-2894(1991).  
RN [4]
- SEQUENCE FROM N.A.  
RN STRAIN=U1102; VARIANT A;  
RC MEDLINE=91133307; PubMed=1651403;  
RA Teo I.A., Griffin B.E., Jones M.D.;  
RT "Characterization of the DNA polymerase gene of human herpesvirus 6.;"  
RL J. Virol. 65:4670-4680(1991).  
RN [5]
- SEQUENCE FROM N.A.  
RN STRAIN=U1102; VARIANT A;  
RC MEDLINE=91226542; PubMed=1851252;  
RA Thomson B.J., Efstathiou S., Honess R.W.;  
RT "Acquisition of the human adeno-associated virus type-2 rep gene by  
human herpesvirus type-6.;"  
RL Nature 351:78-80(1991).  
RN [6]
- SEQUENCE FROM N.A.  
RN STRAIN=U1102; VARIANT A;  
RC MEDLINE=91134590; PubMed=1654446;  
RA Martin M.E.D., Nicholas J., Thomson B.J., Newman C., Honess R.W.;  
RT "Identification of a transactivating function mapping to the putative  
immediate-early locus of human herpesvirus 6.;"  
RL J. Virol. 65:5381-5390(1991).  
RN [7]
- SEQUENCE FROM N.A.  
RN STRAIN=U1102; VARIANT A;  
RC MEDLINE=9233249; PubMed=1321206;  
RA Efstathiou S., Lawrence G.L., Brown C.M., Barrell B.G.;  
RT "Identification of homologues to the human cytomegalovirus US22 gene  
family in human herpesvirus 6.;"  
RL J. Gen. Virol. 73:1661-1671(1992).  
RN [8]
- SEQUENCE FROM N.A.  
RN STRAIN=U1102; VARIANT A;  
RC MEDLINE=92148942; PubMed=1310766;  
RA Geng Y., Chandran B., Josephs S.P., Wood C.;  
RT "Identification and characterization of a human herpesvirus 6 gene  
promoter.;"  
RL J. Virol. 66:1564-1570(1992).  
RN [9]
- SEQUENCE FROM N.A.  
RN STRAIN=U1102; VARIANT A;  
RC MEDLINE=93091236; PubMed=1333836;  
RA Gompels U.A., Carsi A.L., Sun N., Arrand J.R.;  
RT "Infectivity determinants encoded in a conserved gene block of human  
herpesvirus-6.;"  
RL DNA Seq. 3:25-39(1992).  
RN [10]
- SEQUENCE FROM N.A.  
RN STRAIN=U1102; VARIANT A;  
RC MEDLINE=92260671; PubMed=1374813;  
RA Neipel F., Ellinger K., Fleckenstein B.;  
RT "Gene for the major antigenic structural protein (p100) of human  
herpesvirus 6.;"
- RL J. Virol. 66:3918-3924(1992).  
RN [11]
- SEQUENCE FROM N.A.  
RN STRAIN=U1102; VARIANT A;  
RC MEDLINE=9233248; PubMed=1321205;  
RA Thomson B.J., Honess R.W.;  
RT "The right end of the unique region of the genome of human herpesvirus  
6 U1102 contains a candidate immediate early gene enhancer and a  
homologue of the human cytomegalovirus US22 gene family.;"  
RL J. Gen. Virol. 73:1649-1660(1992).  
RN [12]
- SEQUENCE FROM N.A.  
RN STRAIN=U1102; VARIANT A;  
RC MEDLINE=93187613; PubMed=9383182;  
RA Ellinger K., Neipel F., Ioa-Tomas L., Campadelli-Fiume G.,  
Fleckenstein B.;  
RT "The glycoprotein B homologue of human herpesvirus 6.;"  
RL J. Gen. Virol. 74:495-500(1993).  
RN [13]
- SEQUENCE FROM N.A.  
RN STRAIN=U1102; VARIANT A;  
RC MEDLINE=93224882; PubMed=9385692;  
RA Gompels U.A., Carrigan D.R., Carsi A.L., Arno J.;  
RT "Two groups of human herpesvirus 6 identified by sequence analyses of  
laboratory strains and variants from Hodgkin's lymphoma and bone  
marrow transplant patients.;"  
RL J. Gen. Virol. 74:613-622(1993).  
RN [14]
- SEQUENCE FROM N.A.  
RN STRAIN=U1102; VARIANT A;  
RC MEDLINE=93389439; PubMed=9397282;  
RA Liu D.X., Gompels U.A., Nicholas J., Lelliott C.;  
RT "Identification and expression of the human herpesvirus 6 glycoprotein  
H and interaction with an accessory 40K glycoprotein.;"  
RL J. Gen. Virol. 74:1847-1857(1993).  
RN [15]
- SEQUENCE FROM N.A.  
RN STRAIN=U1102; VARIANT A;  
RC MEDLINE=94025558; PubMed=7692666;  
RA Liu D.X., Gompels U.A., Rao-Tomas L., Campadelli-Fiume G.;  
RT "Human herpesvirus-6 glycoprotein H and L homologs are components of  
the gp100 complex and the gH external domain is the target for  
neutralizing monoclonal antibodies.;"  
RL Virology 197:12-22(1993).  
RN [16]
- SEQUENCE FROM N.A.  
RN STRAIN=U1102; VARIANT A;  
RC MEDLINE=9333170; PubMed=7687803;  
RA Peillet P.E., Sanchez-Martinez D., Dominguez G., Black J.B., Anton E.,  
RA Greenmoyer C., Dambach R.;  
RT "A strongly immunoreactive virion protein of human herpesvirus 6  
variant B strain Z29; identification and characterization of the gene  
and mapping of a variant-specific monoclonal antibody reactive  
epitope.;"  
RL Virology 195:521-531(1993).  
RN [17]
- SEQUENCE FROM N.A.  
RN STRAIN=U1102; VARIANT A;  
RC MEDLINE=9333202; PubMed=7687301;  
RA Pfeiffer B., Bernstein Z.N., Neipel F., Chang C.K., Tirvatnabong S.,  
RA Chandran B.;  
RT "Identification and mapping of the gene encoding the glycoprotein  
complex gp82-gp05 of human herpesvirus 6 and mapping of the  
neutralizing epitope recognized by monoclonal antibodies.;"  
RL J. Virol. 67:4611-4620(1993).  
RN [18]
- SEQUENCE FROM N.A.  
RN STRAIN=U1102; VARIANT A;  
RC MEDLINE=9514698; PubMed=7844567;  
RA Gompels U.A., Macaulay H.A.;  
RT "Characterization of human telomeric repeat sequences from human  
herpesvirus 6 and relationship to replication.;"  
RL J. Gen. Virol. 76:451-458(1995).



RA	Beeson K.Y., Benos P.V., Berman B.P., Blandari D., Boishakov S.,	RESULT 10
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,	ID 09U623
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Centur A., Chandra I.,	09U623 PRELIMINARY; PRT; 58 AA.
RA	Cherry J.M., Cowley S., Dahlke C., Davenport L.B., Davies P.,	AC 09U623
RA	de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,	AC 01-MAY-2000 (TIEMBLrel. 13, last sequence update)
RA	Dodson B., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,	DT 01-MAY-2000 (TIEMBLrel. 13, last sequence update)
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Garg N.S., Gelbart W.M., Glaser K.,	DT 01-OCT-2000 (TIEMBLrel. 15, last annotation update)
RA	Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaser K.,	DE METAJOTHINEIN
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,	OS pacifastacus leniusculus (Signal crayfish).
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,	OC Eukaryota; Metzcoa; Arthropoda; Crustacea; Malacostraca; Bivalacra; Eucerida; Decapoda; Plectyemata; Astacidae; Astacoidea; Astacidae; Pacifastacus.
RA	Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,	OC
RA	Jalali M., Kalish F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,	OC
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,	OC
RA	Lasko P., Lei Y., Levitzky A.A., Li J., Li Z., Liang Y., Lin X.,	OK NCBI_TaxID=6720;
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,	RN [1]
RA	Merkulov G., Mishina N.V., Mobarry C., Morris J., Moskrajev A.,	RP SEQUENCE FROM N.A.
RA	Mount S.M., Moy M., Murphy L., Murphy D.M., Nelson D.L.,	RC TISSUE="THORACIC GANGLIA";
RA	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclob J.M.,	RA Skorupski P., Dawbarn D.;
RA	Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,	RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RA	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,	EMBL; AF099482; AAF07215; 1;
RA	Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,	DR HSSP; P55949; IDMC.
RA	Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,	DR INTERPRO; IPR002045; -.
RA	Swirski R., Tector J., Turner R., Venter E., Wang A.-H., Wang X.,	DR INTERPRO; IPR00319; -.
RA	Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,	DR PFAM; PF00131; metalthio; 1.
RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.O.A.,	DR PRINTS; PRO0855; MTCRUSTACEAN.
RA	Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,	DR SEQUENCE 58 AA; 6008 MW; 576635ACFB0E5100 CRC64;
RA	Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,	DR
RT	"The genome sequence of <i>Drosophila melanogaster</i> ,"	DR
RL	Science 2007:2185-2195(2000).	DR
DR	EMBL; AE003540; AAF9882.1; -.	DR
DR	EMBL; AE003540; AAF9882.1; -.	DR
SQ	SEQUENCE 821 AA; 89432 MW;	DR
Query Match 100.0%; Score 76; DB 5; Length 821; Best Local Similarity 21.4%; Pred. No. 41; Matches 6; Conservative 22; Mismatches 0; Indels 0; Gaps 0;	Query Match 88.2%; Score 67; DB 5; Length 104; Best Local Similarity 18.5%; Pred. No. 67; Matches 5; Conservative 22; Mismatches 0; Indels 0; Gaps 0;	
QY 1 CXXCXXCXXXXXXCXXCXXCXXC 28	QY 1 CXXCXXCXXXXXXCXXCXXC 27	
Db 669 CMPCSNQCPNSWYVNPCTGCYVYICANCC 696	Db 31 CDKCTSGCKPPSKERCAKTCSSKPCRC 57	
RESULT 9	RESULT 11	
Q16861 ID 016861 PRELIMINARY; PRT; 46 AA.	Q9NLE3 ID 09NLE3 PRELIMINARY; PRT; 104 AA.	
AC 016861; DT 01-NOV-1996 (TIEMBLrel. 01, Created)	AC 09NLE3; DT 01-OCT-2000 (TIEMBLrel. 15, created)	
DT 01-NOV-1996 (TIEMBLrel. 01, last sequence update)	DT 01-OCT-2000 (TIEMBLrel. 15, last sequence update)	
DT 01-AUG-1998 (TIEMBLrel. 07, last annotation update)	DT 01-OCT-2000 (TIEMBLrel. 15, last annotation update)	
DE COSTINE RICH PROTEIN (FRAGMENT).	DE PROBABLE (HHV-6) U1102, VARIANT A DNA, COMPLETE VIRION GENOME (FRAGMENT).	
OS Homo sapiens (Human).	DE LM26_499.	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarhini; Hominida; Homo. [1]	OS Leishmania major.	
OC NCBI_TaxID=564;	OC Bokaryota; Euglenozoa; Kinetoplastida; Trypanosomatida; Leishmania.	
OX NCBI_TaxID=564;	RN [1]	
RN SEQUENCE FROM N.A.	RP STRAIN="FR1EDLN";	
RP SEQUENCE FROM N.A.	RA Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B., DR Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AL160493; CAB98117.1; -.	
RA EMBL; U65332; ARB05010.1; -.	FT NON_TER 1	
RL Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.	SEQUENCE 104 AA; 11240 MW; OAFOCCD76BB93072 CRC64;	
DR EMBL; U65332; ARB05010.1; -.	Query Match 88.2%; Score 67; DB 5; Length 104; Best Local Similarity 18.5%; Pred. No. 67; Matches 5; Conservative 22; Mismatches 0; Indels 0; Gaps 0;	
FT NON_TER 1	QY 2 XCXXCXXCXXXXXXCXXCXXC 28	
RA SEQUENCE 46 AA; 5061 MW;	Db 58 SQCVCVCVCACVVCACVVCVCVC 84	
Query Match 88.2%; Score 67; DB 4; Length 46; Best Local Similarity 18.5%; Pred. No. 41; Matches 5; Conservative 22; Mismatches 0; Indels 0; Gaps 0;	RESULT 12	
QY 2 XCXXCXXCXXXXXXCXXCXXC 28	Q9NMV2 ID Q9NMV2 PRELIMINARY; PRT; 105 AA.	
Db 9 SRCCCCCCCCCCCCCCCCCCCCFC 35	AC Q9NMV2	

DT	01-OCT-2000	(TREMBLREL. 15, Last sequence update)	RA	Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
DT	01-OCT-2000	(TREMBLREL. 15, Last annotation update)	RA	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
DE	PROBABLE (HHV-6) U1102, VARIANT A DNA, COMPLETE VIRION GENOME (FRAGMENT).		RA	Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
DE	LM15.575.		RA	Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA	Leishmania major.		RA	Switskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA	Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.		RA	Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
OC	Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.;		RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
OX	Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.		RA	Ye J., Yeh R.-P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RN	[1]		RA	Zheng X.H., Zhong F.N., Zhan W., Zhou X., Zhu S., Smith H.O.,
RP	SEQUENCE FROM N.A.		RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RC	STRAIN=FRIEDLIN;		RA	"The genome sequence of <i>Drosophila melanogaster</i> .";
RA	MURPHY L., QUAIL M., HARRIS D., RAJANDREAM M., IVENS A., BARRELL B.;		RL	Science 287, 2185-2195 (2000).
RL	Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.		DR	EMBL: AB003531; AAC49644.1; -.
DR	EMBL: AL160371; CAC00458.1; -.		DR	FLYBASE: FBgn003695; CG7489.
FT	NON_TER 1		DR	INTERPRO: IPR000561; -.
FT	NON_TER 105	105	DR	PPM; P01826; TFL; 1.
SQ	SEQUENCE 105 AA; 11011 MW;	800F71927c95886 CRC64;	DR	PROSITE; PS01186; EGF; 2; UNKNOWN-1.
RESULT 13			SQ	SEQUENCE 108 AA; 11885 MW; 49a0c4c25608e67c CRC64;
Q9YUN1	PRELIMINARY;	PRT; 108 AA.	Q9YUN1;	Query Match 88.2%; Score 67; DB 5; Length 105; Best local Similarity 18.5%; Pred. No. 67; Mismatches 5; Conservative 22; Indels 0; Gaps 0;
AC			AC	Best Local Similarity 18.5%; Pred. No. 67; Mismatches 5; Conservative 22; Indels 0; Gaps 0;
DT	01-MAY-2000 (TREMBLREL. 13, Last created)		DT	01-MAY-2000 (TREMBLREL. 13, Last sequence update)
DT	01-JUN-2000 (TREMBLREL. 14, Last annotation update)		DT	01-JUN-2000 (TREMBLREL. 14, Last annotation update)
DE	CG7489 PROTEIN.		DE	CG7489.
GN			GN	
OS	drosophila melanogaster (Fruit fly).		OS	drosophila melanogaster (Fruit fly).
OC	Eukaryota; Metazoa; Anthropoda; Tracheata; Hexapoda; Insecta;		OC	Eukaryota; Metazoa; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriidae; Drosophilidae; Drosophila.
OC			OC	
NCBI_TaxID:7227;			NCBI_TaxID:7227;	
RN			RN	
RP	SEQUENCE FROM N.A.		RP	SEQUENCE FROM N.A.
RC	STRAIN=BERKELEY;		RC	STRAIN=BERKELEY;
RX	MEDLINE:20190006; PubMed=10731132;		RX	MEDLINE:98008911; PubMed=9344646;
RA	Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,		RA	Zhao X.P., Elder J.T.,
RA	Amanaties P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,		RA	"Positional cloning of novel skin-specific genes from the human
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,		RT	epidermal differentiation complex.";
RA	Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,		RT	Genomics 45:250-258 (1997).
RA	Brandon R.C., Rogers V.-H.C., Blazej R.G., Champine M., Pfeiffer B.D.,		DR	EMBL: AP005080; AAB8360.1; -.
RA	Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.C.R., Miklos G.L.G.,		SQ	SEQUENCE 110 AA; 11219 MW; 861096815ED8D9B3 CRC64;
RA	Abrial J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,		Q9YUN1;	Query Match 88.2%; Score 67; DB 5; Length 108; Best Local Similarity 18.5%; Pred. No. 68; Mismatches 5; Conservative 22; Indels 0; Gaps 0;
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,		AC	Best Local Similarity 18.5%; Pred. No. 69; Mismatches 5; Conservative 22; Indels 0; Gaps 0;
RA	Beeson K.Y., Benos B.P., Bhandari D., Bolshakov S.,		DT	01-JUN-1998 (TREMBLREL. 06, Last created)
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,		DT	01-JUN-1998 (TREMBLREL. 06, Last sequence update)
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,		DT	01-JUN-2000 (TREMBLREL. 13, Last annotation update)
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,		DE	CG7489 PROTEIN.
RA	de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,		GN	ACP62F.
RA	Dobson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,			
RA	Durbin R.M., Evans C., Ferraz C., Ferreira S., Fleischmann W.,			
RA	Fosler C., Gabrieli A.E., Garg N.S., Gelbart W., Glasser K.,			
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,			
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J., Harris R.,			
RA	Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeqwan C.,			
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,			
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz C., Kulp D., Lai Z.,			
RA	Lasko P., lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,			
RA	Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,			
RA	Merkulov G., Milstein N.V., Moberg J., Morris J., Moshrefi A.,			
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzyk D.M., Nelson D.L.,			
RA	Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacled J.M.,			

RESULT 14			Q9YUN1	Query Match 88.2%; Score 67; DB 5; Length 108; Best Local Similarity 18.5%; Pred. No. 68; Mismatches 5; Conservative 22; Indels 0; Gaps 0;
Q9YUN1	PRELIMINARY;	PRT; 110 AA.	Q9YUN1;	Query Match 88.2%; Score 67; DB 5; Length 108; Best Local Similarity 18.5%; Pred. No. 68; Mismatches 5; Conservative 22; Indels 0; Gaps 0;
AC			AC	Best Local Similarity 18.5%; Pred. No. 68; Mismatches 5; Conservative 22; Indels 0; Gaps 0;
DT	01-JAN-1998 (TREMBLREL. 05, Created)		DT	01-JAN-1998 (TREMBLREL. 05, Last sequence update)
DT	01-JUN-1998 (TREMBLREL. 06, Last annotation update)		DT	01-JUN-2000 (TREMBLREL. 13, Last annotation update)
DE	SKIN-SPECIFIC PROTEIN.		DE	SKIN-SPECIFIC PROTEIN.
GN			GN	
OS	Homo sapiens (Human).		OS	Homo sapiens (Human).
OC	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		OC	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.		OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX			OX	
NCBI_TaxID:9606;			NCBI_TaxID:9606;	
RN			RN	
RP	SEQUENCE FROM N.A.		RP	SEQUENCE FROM N.A.
RC	TISSUE=SKIN;		RC	TISSUE=SKIN;
RX	MEDLINE:98008911; PubMed=9344646;		RX	MEDLINE:98008911; PubMed=9344646;
RA			RA	
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,		RA	Zhao X.P., Elder J.T.,
RA	Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,		RA	"Positional cloning of novel skin-specific genes from the human
RA	Brandon R.C., Rogers V.-H.C., Blazej R.G., Champine M., Pfeiffer B.D.,		RT	epidermal differentiation complex.";
RA	Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.C.R., Miklos G.L.G.,		RT	Genomics 45:250-258 (1997).
RA	Abrial J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,		DR	EMBL: AP005080; AAB8360.1; -.
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,		SQ	SEQUENCE 110 AA; 11219 MW; 861096815ED8D9B3 CRC64;
RA	Beeson K.Y., Benos B.P., Bhandari D., Bolshakov S.,		Q9YUN1;	Query Match 88.2%; Score 67; DB 4; Length 110; Best Local Similarity 18.5%; Pred. No. 69; Mismatches 5; Conservative 22; Indels 0; Gaps 0;
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,		AC	Best Local Similarity 18.5%; Pred. No. 69; Mismatches 5; Conservative 22; Indels 0; Gaps 0;
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,		DT	01-JUN-1998 (TREMBLREL. 06, Last created)
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,		DT	01-JUN-1998 (TREMBLREL. 06, Last sequence update)
RA	de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,		DT	01-JUN-2000 (TREMBLREL. 13, Last annotation update)
RA	Dobson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,		DE	CG7489 PROTEIN.
RA	Durbin R.M., Evans C., Ferraz C., Ferreira S., Fleischmann W.,		GN	ACP62F.
RA	Fosler C., Gabrieli A.E., Garg N.S., Gelbart W., Glasser K.,			
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,			
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J., Harris R.,			
RA	Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeqwan C.,			
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,			
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz C., Kulp D., Lai Z.,			
RA	Lasko P., lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,			
RA	Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,			
RA	Merkulov G., Milstein N.V., Moberg J., Morris J., Moshrefi A.,			
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzyk D.M., Nelson D.L.,			
RA	Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacled J.M.,			

Search completed: March 1, 2001, 16:22:06  
 Job time: 283 sec

OS Drosophila melanogaster (fruit fly).  
 OC Eukariota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydriidae; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID:7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celunker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blaej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Balwol R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
 RA Glodek A., Busam D.A., Butler H., Cadieu E., Centner A., Chandra I.,  
 RA Cherry J.M., Carley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablo J.B., Deucher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Douc E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin R.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Posler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
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 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CAENYON S; TISSUE=ACCESSORY GLAND;  
 RA Wolfner M.F., Harada H.A., Bertram M.J., Stellick T.J., Kraus K.W.,  
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 DR EMBL: AE003475; AAF47683; 1;  
 DR EMBL: AB5753; AB9597; 1;  
 DR FLYBASE; FlyBase000509; Acp62F.  
 DR INTERPRO; IPR000561; -  
 DR INTRPRO; IPR00291; -  
 DR PFAM; PF01826; TIL; 1.  
 DR PROSITE; PS01186; EGF\_2; UNKNOWN\_1; AAC6FC32291D CRC64;  
 SQ 115 AA; 12570 MW; 4326AAC6FC32291D CRC64;

Query Match 88.2%; Score 67; DB 5; Length 115;  
 Best Local Similarity 18.5%; Prey. No. 71;  
 Matches 5; Conservative 22; Mismatches 0; Indels 0; Gaps 0;  
 Qy 2 XXCXXCXXXXXXCXXCXXCXXC 28  
 ::::|:|:|:|:|:|:|:|:|:|:|:|:|:  
 Db 41 TECPVACPCEYSGNGPCVKMCGAPC 67